

Patent Application US/07/659,408

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: CAPUT, DANIEL
FERRARA, PASCUAL
GUILLEMOT, JEAN-CLAUDE
KAGHAD, MOURAD
LEGOUX, RICHARD
LOISON, GERARD
LARBRE, ELIZABETH
LUPKER, JOHANNES
LEPLATOIS, PASCUAL
SALOME, MARK

(ii) TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
MICRO-ORGANISMS AND TRANSFORMED CELLS

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Foley & Lardner
(B) STREET: 1800 Diagonal Road, Suite 500
(C) CITY: Alexandria
(D) STATE: Virginia
(E) COUNTRY: USA
(F) ZIP: 22313-0299

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/659,408
(B) FILING DATE: 25-APR-1991
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BENT, Stephen A.
(B) REGISTRATION NUMBER: 29,768
(C) REFERENCE/DOCKET NUMBER: 16781/276 BEDL

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703)836-9300
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(C) TELEX: 899149

(2) INFORMATION FOR SEQ ID NO:1:

OK

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Aspergillus flavus

(vii) IMMEDIATE SOURCE:

(B) CLONE: Urate oxidase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ser Ala Val Lys Ala Ala Arg Tyr Gly Lys Asp Asn Val Arg Val Tyr
1 5 10 15

Lys Val His Lys Asp Glu Lys Thr Gly Val Gln Thr Val Tyr Glu Met
20 25 30

Thr Val Cys Val Leu Leu Glu Gly Glu Ile Glu Thr Ser Tyr Thr Lys
35 40 45

Ala Asp Asn Ser Val Ile Val Ala Thr Asp Ser Ile Lys Asn Thr Ile
50 55 60

Tyr Ile Thr Ala Lys Gln Asn Pro Val Thr Pro Pro Glu Leu Phe Gly
65 70 75 80

Ser Ile Leu Gly Thr His Phe Ile Glu Lys Tyr Asn His Ile His Ala
85 90 95

Ala His Val Asn Ile Val Cys His Arg Trp Thr Arg Met Asp Ile Asp
100 105 110

Gly Lys Pro His Pro His Ser Phe Ile Arg Asp Ser Glu Glu Lys Arg
115 120 125

Asn Val Gln Val Asp Val Val Glu Gly Lys Gly Ile Asp Ile Lys Ser
130 135 140

Ser Leu Ser Gly Leu Thr Val Leu Lys Ser Thr Asn Ser Gln Phe Trp
145 150 155 160

Gly Phe Leu Arg Asp Glu Tyr Thr Thr Leu Lys Glu Thr Trp Asp Arg
165 170 175

Ile Leu Ser Thr Asp Val Asp Ala Thr Trp Gln Trp Lys Asn Phe Ser

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107          180          185          190
108
109 Gly Leu Gln Glu Val Arg Ser His Val Pro Lys Phe Asp Ala Thr Trp
110          195          200          205
111
112 Ala Thr Ala Arg Glu Val Thr Leu Lys Thr Phe Ala Glu Asp Asn Ser
113          210          215          220
114
115 Ala Ser Val Gln Ala Thr Met Tyr Lys Met Ala Glu Gln Ile Leu Ala
116          225          230          235          240
117
118 Arg Gln Gln Leu Ile Glu Thr Val Glu Tyr Ser Leu Pro Asn Lys His
119          245          250          255
120
121 Tyr Phe Glu Ile Asp Leu Ser Trp His Lys Gly Leu Gln Asn Thr Gly
122          260          265          270
123
124 Lys Asn Ala Glu Val Phe Ala Pro Gln Ser Asp Pro Asn Gly Leu Ile
125          275          280          285
126
127 Lys Cys Thr Val Gly Arg Ser Ser Leu Lys Ser Lys Leu
128          290          295          300
129 (2) INFORMATION FOR SEQ ID NO:2:
130
131 (i) SEQUENCE CHARACTERISTICS:
132 (A) LENGTH: 302 amino acids
133 (B) TYPE: amino acid
134 (C) STRANDEDNESS: single
135 (D) TOPOLOGY: linear
136
137 (ii) MOLECULE TYPE: protein
138
139 (iii) HYPOTHETICAL: NO
140
141 (vi) ORIGINAL SOURCE:
142 (A) ORGANISM: Aspergillus flavus
143
144 (vii) IMMEDIATE SOURCE:
145 (B) CLONE: Met-Urate oxidase
146
147
148 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
149
150 Met Ser Ala Val Lys Ala Ala Arg Tyr Gly Lys Asp Asn Val Arg Val
151 1          5          10          15
152
153 Tyr Lys Val His Lys Asp Glu Lys Thr Gly Val Gln Thr Val Tyr Glu
154          20          25          30
155
156 Met Thr Val Cys Val Leu Leu Glu Gly Glu Ile Glu Thr Ser Tyr Thr
157          35          40          45
158
159 Lys Ala Asp Asn Ser Val Ile Val Ala Thr Asp Ser Ile Lys Asn Thr

```

Raw Sequence Listing

10/23/91

11:12:09

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	50	55	60
160			
161			
162	Ile Tyr Ile Thr Ala Lys Gln Asn Pro Val Thr Pro Pro Glu Leu Phe		
163	65	70	75 80
164			
165	Gly Ser Ile Leu Gly Thr His Phe Ile Glu Lys Tyr Asn His Ile His		
166		85	90 95
167			
168	Ala Ala His Val Asn Ile Val Cys His Arg Trp Thr Arg Met Asp Ile		
169		100	105 110
170			
171	Asp Gly Lys Pro His Pro His Ser Phe Ile Arg Asp Ser Glu Glu Lys		
172		115	120 125
173			
174	Arg Asn Val Gln Val Asp Val Val Glu Gly Lys Gly Ile Asp Ile Lys		
175		130	135 140
176			
177	Ser Ser Leu Ser Gly Leu Thr Val Leu Lys Ser Thr Asn Ser Gln Phe		
178		145	150 155 160
179			
180	Trp Gly Phe Leu Arg Asp Glu Tyr Thr Thr Leu Lys Glu Thr Trp Asp		
181		165	170 175
182			
183	Arg Ile Leu Ser Thr Asp Val Asp Ala Thr Trp Gln Trp Lys Asn Phe		
184		180	185 190
185			
186	Ser Gly Leu Gln Glu Val Arg Ser His Val Pro Lys Phe Asp Ala Thr		
187		195	200 205
188			
189	Trp Ala Thr Ala Arg Glu Val Thr Leu Lys Thr Phe Ala Glu Asp Asn		
190		210	215 220
191			
192	Ser Ala Ser Val Gln Ala Thr Met Tyr Lys Met Ala Glu Gln Ile Leu		
193		225	230 235 240
194			
195	Ala Arg Gln Gln Leu Ile Glu Thr Val Glu Tyr Ser Leu Pro Asn Lys		
196		245	250 255
197			
198	His Tyr Phe Glu Ile Asp Leu Ser Trp His Lys Gly Leu Gln Asn Thr		
199		260	265 270
200			
201	Gly Lys Asn Ala Glu Val Phe Ala Pro Gln Ser Asp Pro Asn Gly Leu		
202		275	280 285
203			
204	Ile Lys Cys Thr Val Gly Arg Ser Ser Leu Lys Ser Lys Leu		
205		290	295 300
206			

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 906 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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213 (D) TOPOLOGY: linear
214
215 (ii) MOLECULE TYPE: DNA (genomic)
216
217 (vii) IMMEDIATE SOURCE:
218 (B) CLONE: Preferred sequence for expression in
219 prokaryotes
220
221
222 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
223
224 ATGTCTGCGG TAAAAGCAGC GCGCTACGGC AAGGACAATG TTCGCGTCTA CAAGGTTCAC 60
225
226 AAGGACGAGA AGACCGGTGT CCAGACGGTG TACGAGATGA CCGTCTGTGT GCTTCTGGAG 120
227
228 GGTGAGATTG AGACCTCTTA CACCAAGGCC GACAACAGCG TCATTGTGCGC AACCGACTCC 180
229
230 ATTAAGAACA CCATTTACAT CACCGCCAAG CAGAACCCCG TTAATCCTCC CGAGCTGTTC 240
231
232 GGCTCCATCC TGGGCACACA CTTCAATGAG AAGTACAACC ACATCCATGC CGCTCACGTC 300
233
234 AACATTGTCT GCCACCGCTG GACCCGGATG GACATTGACG GCAAGCCACA CCCTCACTCC 360
235
236 TTCATCCGCG ACAGCGAGGA GAAGCGGAAT GTGCAGGTGG ACGTGGTCTGA GGGCAAGGGC 420
237
238 ATCGATATCA AGTCGTCTCT GTCCGGCCTG ACCGTGCTGA AGAGCACCAA CTCGCAGTTC 480
239
240 TGGGGCTTCC TGCCTGACGA GTACACCACA CTTAAGGAGA CCTGGGACCG TATCCTGAGC 540
241
242 ACCGACGTCG ATGCCACTTG GCAGTGGAAAG AATTTAGTG GACTCCAGGA GGTCCGCTCG 600
243
244 CACGTGCCTA AGTTCGATGC TACCTGGGCC ACTGCTCGCG AGGTCACTCT GAAGACTTTT 660
245
246 GCTGAAGATA ACAGTGCCAG CGTGCAGGCC ACTATGTACA AGATGGCAGA GCAAATCCTG 720
247
248 GCGCGCCAGC AGCTGATCGA GACTGTGCGAG TACTCGTTGC CTAACAAGCA CTATTTTCGAA 780
249
250 ATCGACCTGA GCTGGCACAA GGGCCTCCAA AACACCGGCA AGAACGCCGA GGTCTTCGCT 840
251
252 CCTCAGTCGG ACCCCAACGG TCTGATCAAG TGTACCGTCG GCCGGTCCTC TCTGAAGTCT 900
253
254 AAATTG 906
255
256 (2) INFORMATION FOR SEQ ID NO:4:
257 (i) SEQUENCE CHARACTERISTICS:
258 (A) LENGTH: 906 base pairs
259 (B) TYPE: nucleic acid
260 (C) STRANDEDNESS: single
261 (D) TOPOLOGY: linear
262
263 (ii) MOLECULE TYPE: DNA (genomic)
264
265

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266 (vii) IMMEDIATE SOURCE:
267 (B) CLONE: Preferred sequence for expression in
268 eukaryotes
269
270 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
271
272 ATGTCTGCTG TTAAGGCTGC TAGATACGGT AAGGACAACG TTAGAGTCTA CAAGGTTTAC 60
273
274 AAGGACGAGA AGACCGGTGT CCAGACGGTG TACGAGATGA CCGTCTGTGT GCTTCTGGAG 120
275
276 GGTGAGATTG AGACCTCTTA CACCAAGGCC GACAACAGCG TCATTGTCGC AACCGACTCC 180
277
278 ATTAAGAACA CCATTTACAT CACCGCCAAG CAGAACCCCG TTAATCCTCC CGAGCTGTTC 240
279
280 GGCTCCATCC TGGGCACACA CTTTATTGAG AAGTACAACC ACATCCATGC CGCTCACGTC 300
281
282 AACATTGTCT GCCACCGCTG GACCCGGATG GACATTGACG GCAAGCCACA CCCTCACTCC 360
283
284 TTCATCCGCG ACAGCGAGGA GAAGCGGAAT GTGCAGGTGG ACGTGGTCGA GGGCAAGGGC 420
285
286 ATCGATATCA AGTCGTCTCT GTCCGGCCTG ACCGTGCTGA AGAGCACCAA CTCGCAGTTC 480
287
288 TGGGGCTTCC TGGGTGACGA GTACACCACA CTTAAGGAGA CCTGGGACCG TATCCTGAGC 540
289
290 ACCGACGTCG ATGCCACTTG GCAGTGGAAG AATTTTCAAGT GACTCCAGGA GGTCCGCTCG 600
291
292 CACGTGCCTA AGTTTCGATGC TACCTGGGCC ACTGCTCGCG AGGTCACTCT GAAGACTTTT 660
293
294 GCTGAAGATA ACAGTGCCAG CGTGCAGGCC ACTATGTACA AGATGGCAGA GCAAATCCTG 720
295
296 GCGCGCCAGC AGCTGATCGA GACTGTGAG TACTCGTTGC CTAACAAGCA CTATTTTCGAA 780
297
298 ATCGACCTGA GCTGGCACAA GGGCCTCCAA AACACCGGCA AGAACGCCGA GGTCTTCGCT 840
299
300 CCTCAGTCGG ACCCCAACGG TCTGATCAAG TGTACCGTCG GCCGGTCCTC TCTGAAGTCT 900
301
302 AAATTG 906
303
304 (2) INFORMATION FOR SEQ ID NO:5:
305
306 (i) SEQUENCE CHARACTERISTICS:
307 (A) LENGTH: 14 base pairs
308 (B) TYPE: nucleic acid
309 (C) STRANDEDNESS: single
310 (D) TOPOLOGY: linear
311
312 (ii) MOLECULE TYPE: DNA (genomic)
313
314 (iii) HYPOTHETICAL: NO
315
316
317 (vii) IMMEDIATE SOURCE:
318 (B) CLONE: Preferred non-translated 5' sequence for

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319 animal cells

320

321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

322 AGCTTGCCGC CACT 14

323

324 (2) INFORMATION FOR SEQ ID NO:6:

325

326 (i) SEQUENCE CHARACTERISTICS:

327 (A) LENGTH: 906 base pairs

328 (B) TYPE: nucleic acid

329 (C) STRANDEDNESS: single

330 (D) TOPOLOGY: linear

331

332 (ii) MOLECULE TYPE: DNA (genomic)

333

334 (iii) HYPOTHETICAL: NO

335

336

337 (vii) IMMEDIATE SOURCE:

338 (B) CLONE: Preferred sequence for expression in animal

339 cells

340

341

342 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

343

344 ATGTCCGCAG TAAAAGCAGC CCGCTACGGC AAGGACAATG TCCGCGTCTA CAAGGTTTAC 60

345

346 AAGGACGAGA AGACCGGTGT CCAGACGGTG TACGAGATGA CCGTCTGTGT GCTTCTGGAG 120

347

348 GGTGAGATTG AGACCTCTTA CACCAAGGCC GACAACAGCG TCATTGTGCG AACCGACTCC 180

349

350 ATTAAGAACA CCATTTACAT CACCGCCAAG CAGAACCCCG TTAATCCTCC CGAGCTGTTC 240

351

352 GGCTCCATCC TGGGCACACA CTTTATTGAG AAGTACAACC ACATCCATGC CGCTCACGTC 300

353

354 AACATTGTCT GCCACCGCTG GACCCGGATG GACATTGACG GCAAGCCACA CCCTCACTCC 360

355

356 TTCATCCGCG ACAGCGAGGA GAAGCGGAAT GTGCAGGTGG ACGTGGTCTGA GGGCAAGGGC 420

357

358 ATCGATATCA AGTCGTCTCT GTCCGGCCTG ACCGTGCTGA AGAGCACCAA CTCGCAGTTC 480

359

360 TGGGGCTTCC TCGGTGACGA GTACACCACA CTTAAGGAGA CCTGGGACCG TATCCTGAGC 540

361

362 ACCGACGTCG ATGCCACTTG GCAGTGGAAG AATTTTCAAGT GACTCCAGGA GGTCCGCTCG 600

363

364 CACGTGCCTA AGTTCGATGC TACCTGGGCC ACTGCTCGCG AGGTCACTCT GAAGACTTTT 660

365

366 GCTGAAGATA ACAGTGCCAG CGTGCAGGCC ACTATGTACA AGATGGCAGA GCAAATCCTG 720

367

368 GCGCGCCAGC AGCTGATCGA GACTGTGAG TACTCGTTGC CTAACAAGCA CTATTTTCGAA 780

369

370 ATCGACCTGA GCTGGCACAA GGGCCTCCAA AACACCGGCA AGAACGCCGA GGTCTTCGCT 840

371

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372 CCTCAGTCGG ACCCCAACGG TCTGATCAAG TGTACCGTCG GCCGGTCCTC TCTGAAGTCT 900

373

374 AAATTG 906

375

376 (2) INFORMATION FOR SEQ ID NO:7:

377

(i) SEQUENCE CHARACTERISTICS:

379 (A) LENGTH: 23 base pairs

380 (B) TYPE: nucleic acid

381 (C) STRANDEDNESS: single

382 (D) TOPOLOGY: linear

383

384 (ii) MOLECULE TYPE: DNA (genomic)

385 (iii) HYPOTHETICAL: NO

386

387

388 (vii) IMMEDIATE SOURCE:

389 (B) CLONE: reverse transcription primer

390

391

392 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

393

394 GATCCGGGCC CTTTTTTTTT TTT

23

395

396 (2) INFORMATION FOR SEQ ID NO:8:

397

(i) SEQUENCE CHARACTERISTICS:

399 (A) LENGTH: 10 amino acids

400 (B) TYPE: amino acid

401 (C) STRANDEDNESS: single

402 (D) TOPOLOGY: linear

403

(ii) MOLECULE TYPE: peptide

405

(iii) HYPOTHETICAL: NO

407

408

(vii) IMMEDIATE SOURCE:

410 (B) CLONE: Hydrolysis product T 17

411

412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

414

Asn Val Gln Val Asp Val Val Glu Gly Lys

416 1 5 10

417

(2) INFORMATION FOR SEQ ID NO:9:

419

(i) SEQUENCE CHARACTERISTICS:

421 (A) LENGTH: 8 amino acids

422 (B) TYPE: amino acid

423 (C) STRANDEDNESS: single

424 (D) TOPOLOGY: linear

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425
426 (ii) MOLECULE TYPE: peptide
427
428 (iii) HYPOTHETICAL: NO
429
430 (vii) IMMEDIATE SOURCE:
431 (B) CLONE: Hydrolysis product T 20
432
433
434 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
435
436 Asn Phe Ser Gly Leu Gln Glu Val
437 1 5
438
439 (2) INFORMATION FOR SEQ ID NO:10:
440
441 (i) SEQUENCE CHARACTERISTICS:
442 (A) LENGTH: 6 amino acids
443 (B) TYPE: amino acid
444 (C) STRANDEDNESS: single
445 (D) TOPOLOGY: linear
446
447 (ii) MOLECULE TYPE: peptide
448
449 (iii) HYPOTHETICAL: NO
450
451
452 (vii) IMMEDIATE SOURCE:
453 (B) CLONE: Hydrolysis product T 23
454
455
456 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
457
458 Phe Asp Ala Thr Trp Ala
459 1 5
460
461 (2) INFORMATION FOR SEQ ID NO:11:
462
463 (i) SEQUENCE CHARACTERISTICS:
464 (A) LENGTH: 8 amino acids
465 (B) TYPE: amino acid
466 (C) STRANDEDNESS: single
467 (D) TOPOLOGY: linear
468
469 (ii) MOLECULE TYPE: peptide
470
471 (iii) HYPOTHETICAL: NO
472
473
474 (vii) IMMEDIATE SOURCE:
475 (B) CLONE: Hydrolysis product T 27
476
477

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478 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
479
480 His Tyr Phe Glu Ile Asp Leu Ser
481 1 5
482

483 (2) INFORMATION FOR SEQ ID NO:12:
484
485 (i) SEQUENCE CHARACTERISTICS:
486 (A) LENGTH: 13 amino acids
487 (B) TYPE: amino acid
488 (C) STRANDEDNESS: single
489 (D) TOPOLOGY: linear
490
491 (ii) MOLECULE TYPE: peptide
492
493 (iii) HYPOTHETICAL: NO
494
495
496 (vii) IMMEDIATE SOURCE:
497 (B) CLONE: Hydrolysis product T 28
498
499

500 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
501
502 Ile Leu Ser Thr Asp Val Asp Ala Thr Trp Gln Trp Lys
503 1 5 10
504

505 (2) INFORMATION FOR SEQ ID NO:13:
506
507 (i) SEQUENCE CHARACTERISTICS:
508 (A) LENGTH: 11 amino acids
509 (B) TYPE: amino acid
510 (C) STRANDEDNESS: single
511 (D) TOPOLOGY: linear
512
513 (ii) MOLECULE TYPE: peptide
514
515 (iii) HYPOTHETICAL: NO
516
517
518 (vii) IMMEDIATE SOURCE:
519 (B) CLONE: Hydrolysis product T 29
520
521

522 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
523
524 His Tyr Phe Glu Ile Asp Leu Ser Trp His Lys
525 1 5 10
526

527 (2) INFORMATION FOR SEQ ID NO:14:
528
529 (i) SEQUENCE CHARACTERISTICS:
530 (A) LENGTH: 11 amino acids

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531 (B) TYPE: amino acid
532 (C) STRANDEDNESS: single
533 (D) TOPOLOGY: linear
534
535 (ii) MOLECULE TYPE: peptide
536
537 (iii) HYPOTHETICAL: NO
538
539
540 (vii) IMMEDIATE SOURCE:
541 (B) CLONE: Hydrolysis product T 31
542
543
544 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
545
546 Ser Thr Asn Ser Gln Phe Trp Gly Phe Leu Arg
547 1 5 10
548
549 (2) INFORMATION FOR SEQ ID NO:15:
550
551 (i) SEQUENCE CHARACTERISTICS:
552 (A) LENGTH: 16 amino acids
553 (B) TYPE: amino acid
554 (C) STRANDEDNESS: single
555 (D) TOPOLOGY: linear
556
557 (ii) MOLECULE TYPE: peptide
558
559 (iii) HYPOTHETICAL: NO
560
561
562 (vii) IMMEDIATE SOURCE:
563 (B) CLONE: Hydrolysis product T 32
564
565
566 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
567
568 Gln Asn Pro Val Thr Pro Pro Glu Leu Phe Gly Ser Ile Leu Gly Thr
569 1 5 10 15
570
571
572 (2) INFORMATION FOR SEQ ID NO:16:
573
574 (i) SEQUENCE CHARACTERISTICS:
575 (A) LENGTH: 16 amino acids
576 (B) TYPE: amino acid
577 (C) STRANDEDNESS: single
578 (D) TOPOLOGY: linear
579
580 (ii) MOLECULE TYPE: peptide
581
582 (iii) HYPOTHETICAL: NO
583

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584

585 (vii) IMMEDIATE SOURCE:

586 (B) CLONE: Hydrolysis product T 33

587

588

589 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

590

591 Gln Asn Pro Val Thr Pro Pro Glu Leu Phe Gly Ser Ile Leu Gly Thr

592 1 5 10 15

593

594

595 (2) INFORMATION FOR SEQ ID NO:17:

596

597 (i) SEQUENCE CHARACTERISTICS:

598 (A) LENGTH: 25 amino acids

599 (B) TYPE: amino acid

600 (C) STRANDEDNESS: single

601 (D) TOPOLOGY: linear

602

603 (ii) MOLECULE TYPE: peptide

604

605 (iii) HYPOTHETICAL: NO

606

607

608 (vii) IMMEDIATE SOURCE:

609 (B) CLONE: Hydrolysis product V 1

610

611

612 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

613

614 Tyr Ser Leu Pro Asn Lys Ala Asp Asn Ser Val Ile Val Asp Thr Asp

615 1 5 10 15

616

617 Ser Ile Lys Asn Thr Ile Tyr Ile Thr

618 20 25

619

620 (2) INFORMATION FOR SEQ ID NO:18:

621

622 (i) SEQUENCE CHARACTERISTICS:

623 (A) LENGTH: 16 amino acids

624 (B) TYPE: amino acid

625 (C) STRANDEDNESS: single

626 (D) TOPOLOGY: linear

627

628 (ii) MOLECULE TYPE: peptide

629

630 (iii) HYPOTHETICAL: NO

631

632

633 (vii) IMMEDIATE SOURCE:

634 (B) CLONE: Hydrolysis product V 2

635

636

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637 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

638

639 Val Thr Leu Lys Thr Phe Ala Glu Asp Asn Ser Ala Ser Val Gln Ala

640 1 5 10 15

641

642 (2) INFORMATION FOR SEQ ID NO:19:

643

644 (i) SEQUENCE CHARACTERISTICS:

645 (A) LENGTH: 24 amino acids

646 (B) TYPE: amino acid

647 (C) STRANDEDNESS: single

648 (D) TOPOLOGY: linear

649

650 (ii) MOLECULE TYPE: peptide

651

652 (iii) HYPOTHETICAL: NO

653

654

655 (vii) IMMEDIATE SOURCE:

656 (B) CLONE: Hydrolysis product V 3

657

658

659 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

660

661 Thr Ser Tyr Thr Lys Ala Asp Asn Ser Val Ile Val Asp Thr Asp Ser

662 1 5 10 15

663

664 Ile Lys Asn Thr Ile Tyr Ile Thr

665 20

666

667 (2) INFORMATION FOR SEQ ID NO:20:

668

669 (i) SEQUENCE CHARACTERISTICS:

670 (A) LENGTH: 28 amino acids

671 (B) TYPE: amino acid

672 (C) STRANDEDNESS: single

673 (D) TOPOLOGY: linear

674

675 (ii) MOLECULE TYPE: peptide

676

677 (iii) HYPOTHETICAL: NO

678

679

680 (vii) IMMEDIATE SOURCE:

681 (B) CLONE: Hydrolysis product V 5

682

683

684 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

685

686 Gly Lys Gly Ile Asp Ile Lys Ser Ser Leu Ser Gly Leu Thr Val Leu

687 1 5 10 15

688

689 Lys Ser Thr Asn Ser Gln Phe Trp Gly Phe Leu Arg

#6

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690 20 25
691
692 (2) INFORMATION FOR SEQ ID NO:21:
693
694 (i) SEQUENCE CHARACTERISTICS:
695 (A) LENGTH: 17 amino acids
696 (B) TYPE: amino acid
697 (C) STRANDEDNESS: single
698 (D) TOPOLOGY: linear
699
700 (ii) MOLECULE TYPE: peptide
701
702 (iii) HYPOTHETICAL: NO
703
704 (vii) IMMEDIATE SOURCE:
705 (B) CLONE: Hydolysis product V 6
706
707
708
709 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
710
711 Gly Lys Gly Ile Asp Ile Lys Ser Ser Leu Ser Gly Leu Thr Val Leu
712 1 5 10 15
713
714 Lys
715
716
717 (2) INFORMATION FOR SEQ ID NO:22:
718
719 (i) SEQUENCE CHARACTERISTICS:
720 (A) LENGTH: 1236 base pairs
721 (B) TYPE: nucleic acid
722 (C) STRANDEDNESS: single
723 (D) TOPOLOGY: linear
724
725 (ii) MOLECULE TYPE: DNA (genomic)
726
727 (iii) HYPOTHETICAL: NO
728
729 (vii) IMMEDIATE SOURCE:
730 (B) CLONE: Fragment 3
731
732
733
734 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
735
736 GATCCGCGGA AGCATAAAGT GTAAAGCCTG GGGTGCCTAA TGAGTGAGCT AACTTACATT 60
737
738 AATTGCGTTG CGCTCACTGC CCGCTTTCCA GTCGGGAAAC CTGTCGTGCC AGCTGCATTA 120
739
740 ATGAATCGGC CAACGCGCGG GGAGAGGCGG TTTGCGTATT GGGCGCCAGG GTGGTTTTTC 180
741
742 TTTTCACCAG TGAGACGGGC AACAGCTGAT TGCCCTTCAC CGCCTGGCCC TGAGAGAGTT 240

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743
744 GCAGCAAGCG GTCCACGCTG GTTTGCCCCA CCACCCGAAA ATCCTGTTTG ATGGTGGTTA 300
745
746 ACGGCGGGAT ATAACATGAG CTGTCTTCGG TATCGTCGTA TCCCACTACC GAGATATCCG 360
747
748 CACCAACGCG CAGCCCGGAC TCGGTAATGG CGCGCATTGC GCCCAGCGCC ATCTGATCGT 420
749
750 TGGCAACCAG CATCGCAGTG GGAACGATGC CCTCATTGAG CATTTGCATG GTTTGTTGAA 480
751
752 AACC GGACAT GGC ACTCCAG TCGCCTTCCC GTTCCGCTAT CGGCTGAATT TGATTGCGAG 540
753
754 TGAGATATTT ATGCCAGCCA GCCAGACGCA GACGCGCCGA GACAGAACTT AATGGGCCCCG 600
755
756 CTAACAGCGC GATTTGCTGG TGACCCAATG CGACCAGATG CTCCACGCCC AGTCGCGTAC 660
757
758 CGTCTTCATG GGAGAAAATA ATACTGTTGA TGGGTGTCTG GTCAGAGACA TCAAGAAATA 720
759
760 ACGCCGGAAC ATTAGTGAG GCAGCTTCCA CAGCAATGGC ATCCTGGTCA TCCAGCGGAT 780
761
762 AGTTAATGAT CAGCCCACTG ACGCGTTGCG CGAGAAGATT GTGCACCGCC GCTTTACAGG 840
763
764 CTTGACGCGC GCTTCGTTCT ACCATCGACA CCACCACGCT GGCACCCAGT TGATCGGCGC 900
765
766 GAGATTTAAT CGCCGCGACA ATTTGCGACG GCGCGTGAGG GGCCAGACTG GAGGTGGCAA 960
767
768 CGCCAATCAG CAACGACTGT TTGCCCCGCA GTTGTGTGTC CACGCGGTTG GGAATGTAAT 1020
769 TCAGCTCCGC CATCGCCGCT TCCACTTTTT CCCGCGTTTT CGCAGAAACG TGGCTGGCCT 1080
770
771 GGTTCACCAC GCGGGAAACG GTCTGATAAC AGACACCGGC ATACTCTGCG ACATCGTATA 1140
772
773 ACGTTACTGG TTTCACATTC ACCACCCTGA ATTGACTCTC TTCCGGGCGC TATCATGCCA 1200
774
775 TACCGCGAAA GGTTTTGGCG CATTCGATGG TGTCCG 1236
776

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Fragment 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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796 TCGAGCTGAC TGACCTGTTG CTTATATTAC ATCGATAGCT TAGCGTATAA TGTGTGGAAT 60
797
798 TGTGAGCGAT AACAAATTCA CACAGTTTAA CTTTAAGAAG GAGATATACA TATGGCTACC 120
799
800 GGATCCCGGA CTAGTCTGCT CCTGGCTTTT GGCCTGCTCT GCCTGCCCTG GCTTCAAGAG 180
801
802 GGCAGTGCCT TCCCAACCAT TCCCTTATCT AGACTTTTTG ACAACGCTAT GCTCCGCGCC 240
803
804 CATCGTCTGC ACCAGCTGGC CTTTGACACC TACCAGGAGT TTGAAGAAGC CTATATCCCA 300
805 AAGGAACAGA AGTATTCATT CCTGCA 326
806

807 (2) INFORMATION FOR SEQ ID NO:24:

808

809 (i) SEQUENCE CHARACTERISTICS:

810 (A) LENGTH: 74 base pairs

811 (B) TYPE: nucleic acid

812 (C) STRANDEDNESS: single

813 (D) TOPOLOGY: linear

814

815 (ii) MOLECULE TYPE: DNA (genomic)

816

817 (iii) HYPOTHETICAL: NO

818

819

820 (vii) IMMEDIATE SOURCE:

821 (B) CLONE: ClaI-NdeI fragment

822

823

824 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

825

826 CGATAGCGTA TAATGTGTGG AATTGTGAGC GGATAACAAT TTCACACAGT TTTTCGCGAA 60

827

828 GAAGGAGATA TACA 74

829

830 (2) INFORMATION FOR SEQ ID NO:25:

831

832 (i) SEQUENCE CHARACTERISTICS:

833 (A) LENGTH: 163 base pairs

834 (B) TYPE: nucleic acid

835 (C) STRANDEDNESS: single

836 (D) TOPOLOGY: linear

837

838 (ii) MOLECULE TYPE: DNA (genomic)

839

840 (iii) HYPOTHETICAL: NO

841

842

843 (vii) IMMEDIATE SOURCE:

844 (B) CLONE: Synthetic hGH gene end fragment

845

846

847 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

848

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849 GATCTTCAAG CAGACCTACA GCGACGCACT ACTCAAGAAC TACGGGCTGC TCTACTGCTT 60
850
851 CAGGAAGGAC ATGGACAAGG TCGAGACATT CCTGCGCATC GTGCAGTGCC GCTCTGTGGA 120
852
853 GGGCAGCTGT GGCTTCTAGT AAGGTACCCT GCCCTACGTA CCA 163
854
855 (2) INFORMATION FOR SEQ ID NO:26:
856
857 (i) SEQUENCE CHARACTERISTICS:
858 (A) LENGTH: 48 base pairs
859 (B) TYPE: nucleic acid
860 (C) STRANDEDNESS: single
861 (D) TOPOLOGY: linear
862
863 (ii) MOLECULE TYPE: DNA (genomic)
864
865 (iii) HYPOTHETICAL: NO
866
867
868 (vii) IMMEDIATE SOURCE:
869 (B) CLONE: NdeI-AccII synthetic fragment
870
871
872 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
873
874 TATGTCTGCG GTAAAAGCAG CGCGCTACGG CAAGGACAAT GTTCGCGT 48
875
876 (2) INFORMATION FOR SEQ ID NO:27:
877
878 (i) SEQUENCE CHARACTERISTICS:
879 (A) LENGTH: 361 base pairs
880 (B) TYPE: nucleic acid
881 (C) STRANDEDNESS: single
882 (D) TOPOLOGY: linear
883
884 (ii) MOLECULE TYPE: DNA (genomic)
885
886 (iii) HYPOTHETICAL: NO
887
888
889 (vii) IMMEDIATE SOURCE:
890 (B) CLONE: Plasmid pEMR469 fragment with ADH2 promoter
891
892
893 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
894
895 GGGACGCGTC TCCTCTGCCG GAACACCGGG CATCTCCAAC TTATAAGTTG GAGAAATAAG 60
896
897 AGAATTTTCAG ATTGAGAGAA TGAAAAAAAAA AAAAAAAAAA AAGGCAGAGG AGAGCATAGA 120
898
899 AATGGGGTTC ACTTTTTGGT AAAGCTATAG CATGCCTATC ACATATAAAT AGAGTGCCAG 180
900
901 TAGCGACTTT TTTCACACTC GAGATACTCT TACTACTGCT CTCTTGTTGT TTTTATCACT 240

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902
903 TCTTGTCTTCT TCTTTGGTAA ATAGAATATC AAGCTACAAA AAGCATACAA TCAACTATCA 300
904
905 ACTATTAACT ATATCGATAC CATATGGATC CGTCGACTCT AGAGGATCGT CGACTCTAGA 360
906
907 G 361
908
909 (2) INFORMATION FOR SEQ ID NO:28:
910
911 (i) SEQUENCE CHARACTERISTICS:
912 (A) LENGTH: 58 base pairs
913 (B) TYPE: nucleic acid
914 (C) STRANDEDNESS: single
915 (D) TOPOLOGY: linear
916
917 (ii) MOLECULE TYPE: DNA (genomic)
918
919 (iii) HYPOTHETICAL: NO
920
921
922 (vii) IMMEDIATE SOURCE:
923 (B) CLONE: Fragment C
924
925
926 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
927
928 CGATATACAC AATGTCTGCT GTTAAGGCTG CTAGATACGG TAAGGACAAC GTTAGAGT 58
929
930 (2) INFORMATION FOR SEQ ID NO:29:
931
932 (i) SEQUENCE CHARACTERISTICS:
933 (A) LENGTH: 1013 base pairs
934 (B) TYPE: nucleic acid
935 (C) STRANDEDNESS: single
936 (D) TOPOLOGY: linear
937
938 (ii) MOLECULE TYPE: DNA (genomic)
939
940 (iii) HYPOTHETICAL: NO
941
942
943 (vii) IMMEDIATE SOURCE:
944 (B) CLONE: Fragment D
945
946
947 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
948
949 CTACAAGGTT CACAAGGACC ACAAGACCGG TGTCCAGACG GTGTACGAGA TGACCGTCTG 60
950
951 TGTGCTTCTG GAGGGTGAGA TTGAGACCTC TTACACCAAG GCCGACAACA GCGTCATTGT 120
952
953 CGCAACCGAC TCCATTAAAG ACACCATTTA CATCACCGCC AAGCAGAACC CCGTTACTCC 180
954

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955 TCCCGAGCTG TTCGGCTCCA TCCTGGGCAC ACACCTTCAT TGAGAAGTAC AACACATCCA 240
956
957 TGCCGCTCAC GTCAACATTG TCTGCCACCG CTGGACCCGG ATGGACATTG ACGGCAAGCC 300
958
959 ACACCCTCAC TCCTTCATCC GCGACAGCGA GGAGAAGCGG AATGTGCAGG TGGACGTGGT 360
960
961 CGAGGGCAAG GGCATCGATA TCAAGTCGTC TCTGTCCGGC CTGACCGTGC TGAAGAGCAC 420
962
963 CAACTCGCAG TTCTGGGGCT TCCTGCGTGA CGAGTACACC ACACCTAAGG AGACCTGGGA 480
964
965 CCGTATCCTG AGCACCGACG TCGATGCCAC TTGGCAGTGG AAGAATTTCA GTGGACTCCA 540
966
967 GGAGGTCCGC TCGCACGTGC CTAAGTTCGA TGCTACCTGG GCCACTGCTC GCGAGGTCAC 600
968
969 TCTGCCGACT TTGCTGAAG ATAACAGTGC CAGCGTCAG GCCACTATGT ACAAGATGGC 660
970
971 AGAGCAAATC CTGGCGCGCC AGCAGCTGAT CGAGACTGTC GAGTACTCGT TGCCTAACAA 720
972
973 GCACTATTTT GAAATCGACC TGAGCTGGCA CAAGGGCCTC CAAAACACCG GCAAGAACGC 780
974
975 CGAGGTCTTC GCTCCTCAGT CGGACCCCAA CGGTCTGATC AAGTGTACCG TCGGCCGGTC 840
976
977 CTCTCTGAAG TCTAAATTGT AAACCAACAT GATTCTCACG TTCCGGAGTT TCCAAGGCAA 900
978
979 ACTGTATATA GTCTGGGATA GGGTATAGCA TTCATTCACT TGTTTTTTTAC TTCCAAAAAA 960
980
981 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGGGC CCG 1013
982
983 (2) INFORMATION FOR SEQ ID NO:30:
984
985 (i) SEQUENCE CHARACTERISTICS:
986 (A) LENGTH: 207 base pairs
987 (B) TYPE: nucleic acid
988 (C) STRANDEDNESS: single
989 (D) TOPOLOGY: linear
990
991 (ii) MOLECULE TYPE: DNA (genomic)
992
993 (iii) HYPOTHETICAL: NO
994
995
996 (vii) IMMEDIATE SOURCE:
997 (B) CLONE: Synthetic GAL7 fragment
998
999
1000 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
1001
1002 CGCGTCTATA CTTCGGAGCA CTGTTGAGCG AAGGCTCATT AGATATATTT TCTGTCATTT 60
1003
1004 TCCTTAACCC AAAAATAAGG GAGAGGGTCC AAAAAGCGCT CGGACAACTG TTGACCGTGA 120
1005
1006 TCCGAAGGAC TGGCTATACA GTGTTCAACA AATAGCCAAG CTGAAAATAA TGTGTAGCCT 180
1007

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1008 TTAGCTATGT TCAGTTAGTT TGGCATG 207
1009
1010 (2) INFORMATION FOR SEQ ID NO:31:
1011
1012 (i) SEQUENCE CHARACTERISTICS:
1013 (A) LENGTH: 23 base pairs
1014 (B) TYPE: nucleic acid
1015 (C) STRANDEDNESS: single
1016 (D) TOPOLOGY: linear
1017
1018 (ii) MOLECULE TYPE: DNA (genomic)
1019
1020 (iii) HYPOTHETICAL: NO
1021
1022 (vii) IMMEDIATE SOURCE:
1023 (B) CLONE: Modified XbaI-MluI adapter
1024
1025 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
1026
1027 CTAGGCTAGC GGGCCCCGCAT GCA 23
1028
1029 (2) INFORMATION FOR SEQ ID NO:32:
1030
1031 (i) SEQUENCE CHARACTERISTICS:
1032 (A) LENGTH: 422 base pairs
1033 (B) TYPE: nucleic acid
1034 (C) STRANDEDNESS: single
1035 (D) TOPOLOGY: linear
1036
1037 (ii) MOLECULE TYPE: DNA (genomic)
1038
1039 (iii) HYPOTHETICAL: NO
1040
1041
1042 (vii) IMMEDIATE SOURCE:
1043 (B) CLONE: Plasmid pSE1 "site binding to HindIII"
1044 fragment
1045
1046
1047 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
1048
1049 AGCTGGCTCG CATCTCTCCT TCACGCGCCC GCCGCCCTAC CTGAGGCCGC CATCCACGCC 60
1050
1051 GGTGAGTCGC GTTCTGCCGC CTCCGCGCTG TGGTGCTTCC TGAAGTTCGT CCGCCGTCTA 120
1052
1053 GGTAGGCTCC AAGGGAGCCG GACAAAGGCC CGGTCTCGAC CTGAGCTCTA AACTTACCTA 180
1054
1055 GACTCAGCCG GCTCTCCACG CTTTGCTTGA CCCTGCTTGC TCAACTCTAC GTCTTTGTTT 240
1056
1057 CGTTTTCTGT TCTGCGCCGT TACAACTTCA AGGTATGCGC TGGGACCTGG CAGGCGGCAT 300
1058
1059 CTGGGACCCC TAGGAAGGGC TTGGGGGTCC TCGTGCCCAA GGCAGGGAAC ATAGTGGTCC 360
1060

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1061 CAGGAAGGGG AGCAGAGGCA TCAGGGTGTCT CACTTTGTCT CCGCAGCTCC TGAGCCTGCA 420
1062
1063 GA 422
1064
1065 (2) INFORMATION FOR SEQ ID NO:33:
1066
1067 (i) SEQUENCE CHARACTERISTICS:
1068 (A) LENGTH: 77 base pairs
1069 (B) TYPE: nucleic acid
1070 (C) STRANDEDNESS: single
1071 (D) TOPOLOGY: linear
1072
1073 (ii) MOLECULE TYPE: DNA (genomic)
1074 (iii) HYPOTHETICAL: NO
1075
1076
1077 (vii) IMMEDIATE SOURCE:
1078 (B) CLONE: Synthetic HindIII-"site binding to BamHI"
1079 fragment
1080
1081
1082 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
1083
1084 AGCTTGTCGA CTAATACGAC TCACTATAGG GCGGCCGCGG GCCCCTGCAG GAATTCGGAT 60
1085
1086 CCCCCGGGTG ACTGACT 77
1087
1088 (2) INFORMATION FOR SEQ ID NO:34:
1089 (i) SEQUENCE CHARACTERISTICS:
1090 (A) LENGTH: 61 base pairs
1091 (B) TYPE: nucleic acid
1092 (C) STRANDEDNESS: single
1093 (D) TOPOLOGY: linear
1094
1095 (ii) MOLECULE TYPE: DNA (genomic)
1096
1097 (iii) HYPOTHETICAL: NO
1098
1099
1100 (vii) IMMEDIATE SOURCE:
1101 (B) CLONE: Synthetic HindIII-AccI fragment
1102
1103
1104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
1105
1106 AGCTTGCCGC CACTATGTCC GCAGTAAAAG CAGCCCCTA CCGCAAGGAC AATGTCCGCG 60
1107
1108 T 61
1109
1110 (2) INFORMATION FOR SEQ ID NO:35:
1111
1112 (i) SEQUENCE CHARACTERISTICS:
1113 (A) LENGTH: 920 base pairs

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1114 (B) TYPE: nucleic acid
1115 (C) STRANDEDNESS: single
1116 (D) TOPOLOGY: linear
1117
1118 (ii) MOLECULE TYPE: DNA (genomic)
1119
1120 (iii) HYPOTHETICAL: NO
1121
1122
1123 (vii) IMMEDIATE SOURCE:
1124 (B) CLONE: HindIII-SnaBI fragment
1125
1126
1127 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
1128
1129 AGCTTGCCGC CACTATGTCC GCAGTAAAAG CAGCCCCGCTA CGGCAAGGAC AATGTCCGCG 60
1130
1131 TCTACAAGGT TCACAAGGAC GAGAAGACCG GTGTCCAGAC GGTGTACGAG ATGACCGTCT 120
1132
1133 GTGTGCTTCT GGAGGGTGAG ATTGAGACCT CTTACACCAA GGCCGACAAC AGCGTCATTG 180
1134
1135 TCGCAACCGA CTCCATTAAAG AACACCATTT ACATCACCGC CAAGCAGAAC CCCGTTACTC 240
1136
1137 CTCCCAGAGT GTTCGGCTCC ATCCTGGGCA CACACTTCAT TGAGAAGTAC AACCACATCC 300
1138
1139 ATGCCGCTCA CGTCAACATT GTCTGCCACC GCTGGACCCG GATGGACATT GACGGCAAGC 360
1140
1141 CACACCCTCA CTCCTTCATC CGCGACAGCG AGGAGAAGCG GAATGTGCAG GTGGACGTGG 420
1142
1143 TCGAGGGCAA GGGCATCGAT ATCAAGTCGT CTCTGTCCGG CCTGACCGTG CTGAAGAGCA 480
1144
1145 CCAACTCGCA GTTCTGGGGC TTCCTGCGTG ACGAGTACAC CAACTTAAG GAGACCTGGG 540
1146
1147 ACCGTATCCT GAGCACCGAC GTCGATGCCA CTTGGCAGTG GAAGAATTTT AGTGGACTCC 600
1148
1149 AGGAGGTCCG CTCGCACGTG CCTAAGTTTG ATGCTACCTG GGCCACTGCT CGCGAGGTCA 660
1150
1151 CTCTGAAGAC TTTTGCTGAA GATAACAGTG CCAGCGTGCA GGCCACTATG TACAAGATGG 720
1152
1153 CAGAGCAAAT CCTGGCGCGC CAGCAGCTGA TCGAGACTGT CGAGTACTCG TTGCCTAACA 780
1154
1155 AGCACTATTT CGAAATCGAC CTGAGCTGGC ACAAGGGCCT CAAAACACC GGCAAGAACG 840
1156
1157 CCGAGGTCTT CGCTCCTCAG TCGGACCCCA ACGGTCTGAT CAAGTGTAAC GTCGGCCGGT 900
1158
1159 CCTCTCTGAA GTCTAAATTG 920

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219 Response Exceeds Line Limitations
268 Response Exceeds Line Limitations
319 Response Exceeds Line Limitations
339 Response Exceeds Line Limitations
1044 Response Exceeds Line Limitations
1079 Response Exceeds Line Limitations

(A) APPLICATION NUMBER: US 07/659,408

prokaryotes
eukaryotes
animal cells
cells
fragment
fragment

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